

# aCGHViewer: A Dedicated Viewer for Array CGH Data

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**Buffalo, New York**



# Objectives:

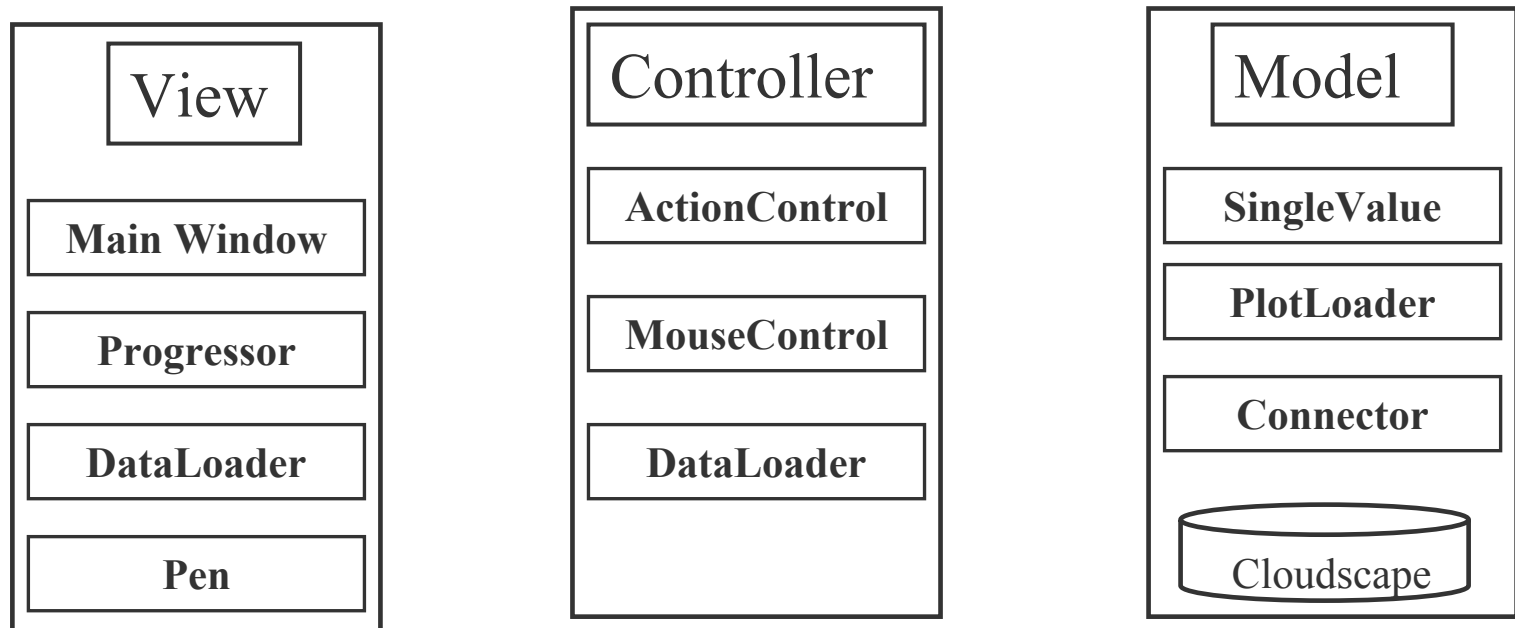
- To develop a dedicated, simple, and easy to use application for viewing/browsing array CGH data

# Functionality Design:

- Data importing, interface for data selection and labeling, selecting of filter, image printing
- Genome-wide viewing (summary plots)
- Detailed analysis of selected genome regions (X-axis zooming)
- Scaling on Y-axis; select data to plot (Y values)
- Link to genome browser for individual data points Side-by-side comparison of multiple samples
- Defining threshold lines, change plot color
- Display of available cytobands on X-axis
- Accommodate all genomes with available genome map data.
- Accommodate all array CGH platforms with genome map information.
- Accommodate plot of expression data along with aCGH data for comparison
- Option to provide other visualization plots
- Implement a statistical analysis package as companion tool

# Development Design

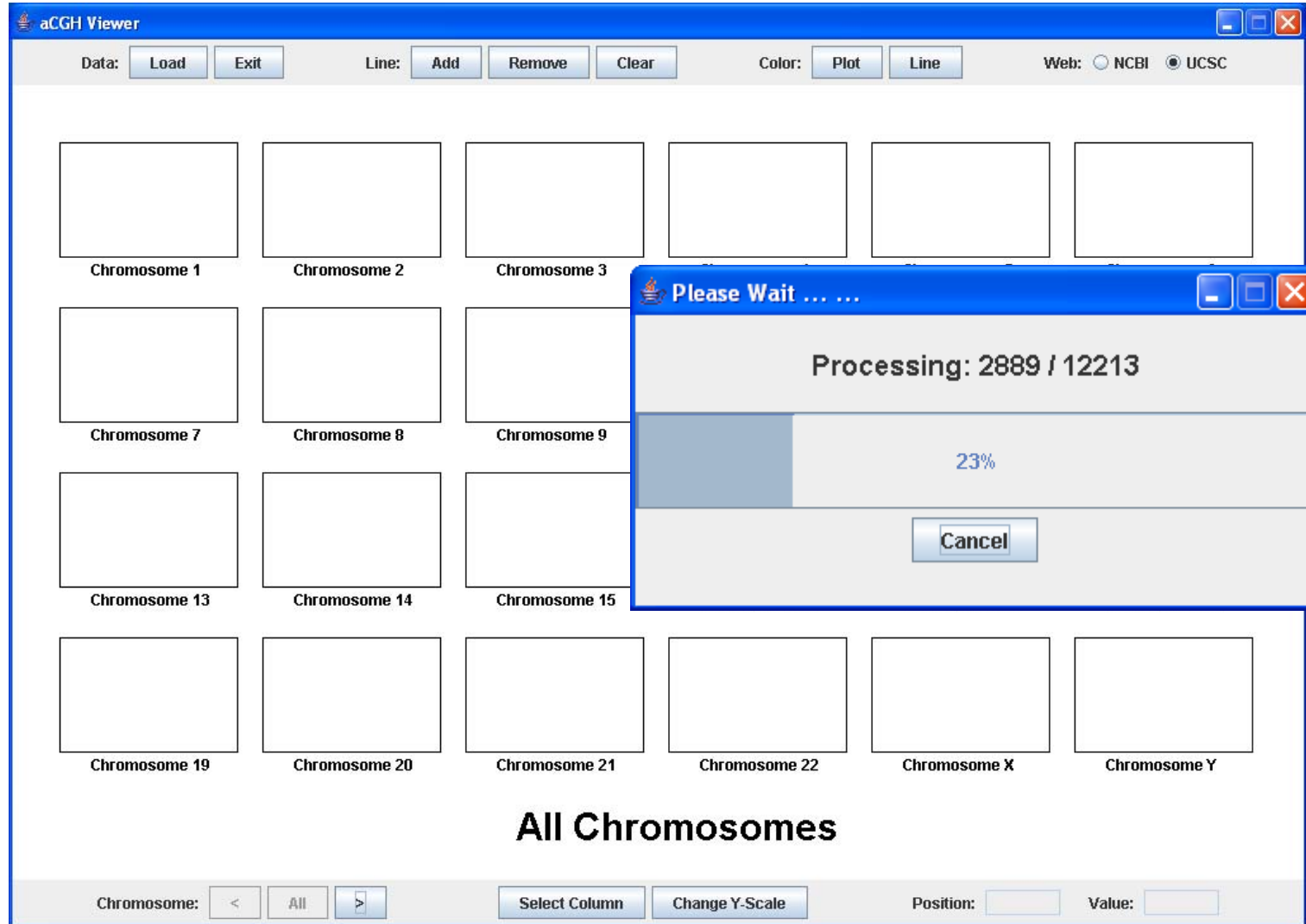
- Standalone Java application, platform independent.
- Implemented using MVC Pattern.
- IBM Cloudscape as embedded database.



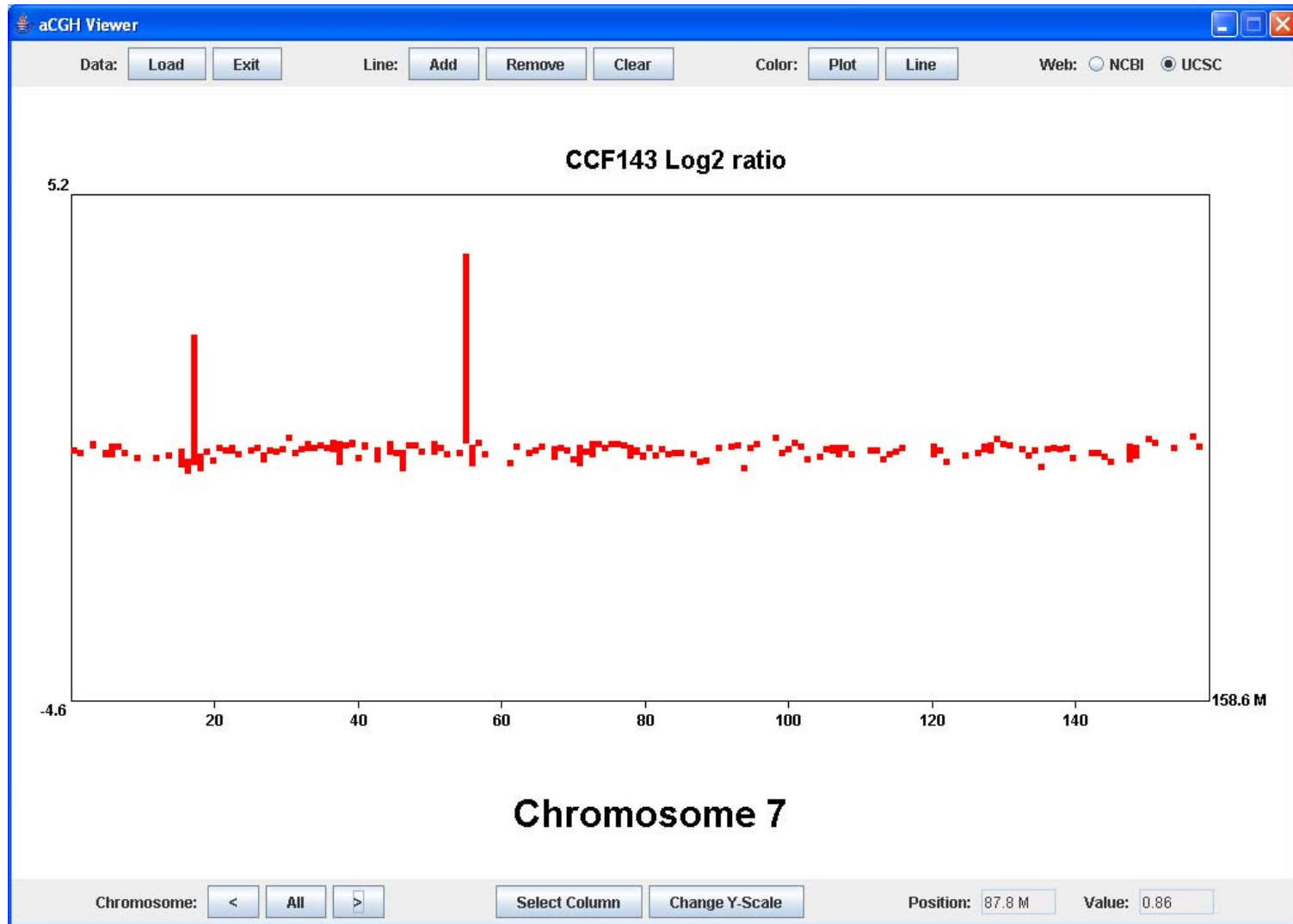
# Currently available functions (in red font)

- **Data importing**, interface for data selection and labeling, selecting of filter, image printing
- Genome-wide viewing (summary plots)
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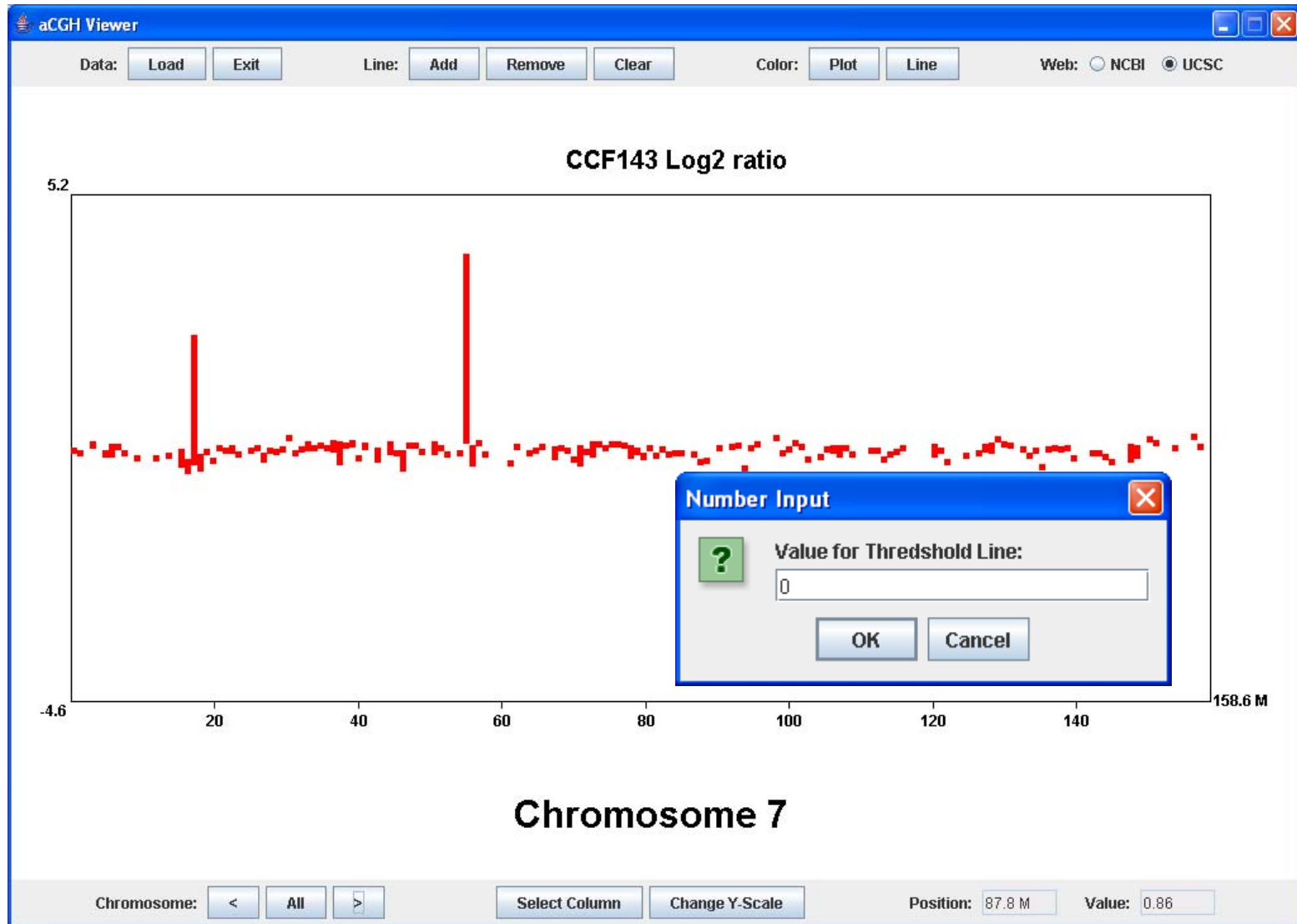
# Data import



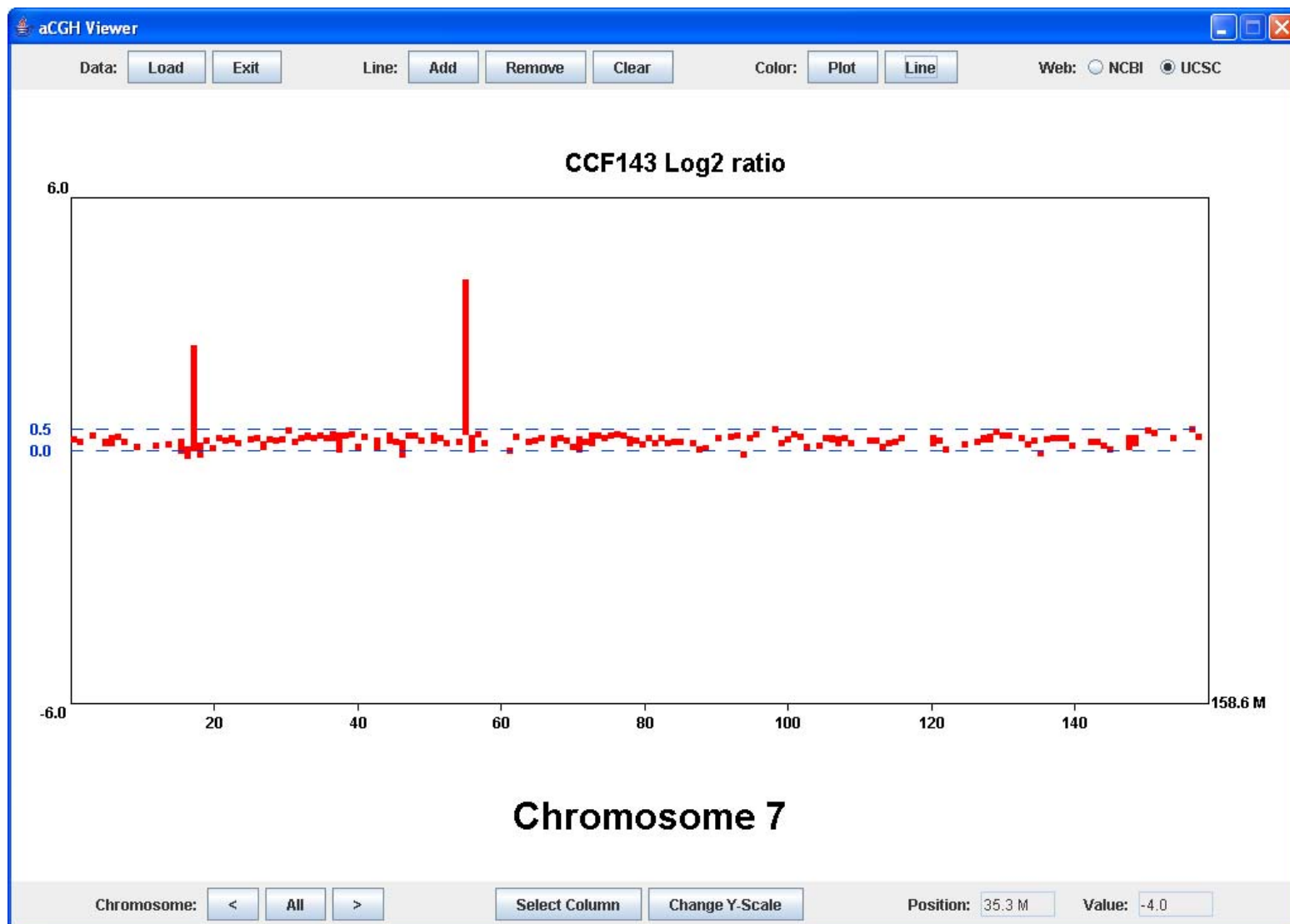
# Individual chromosomes



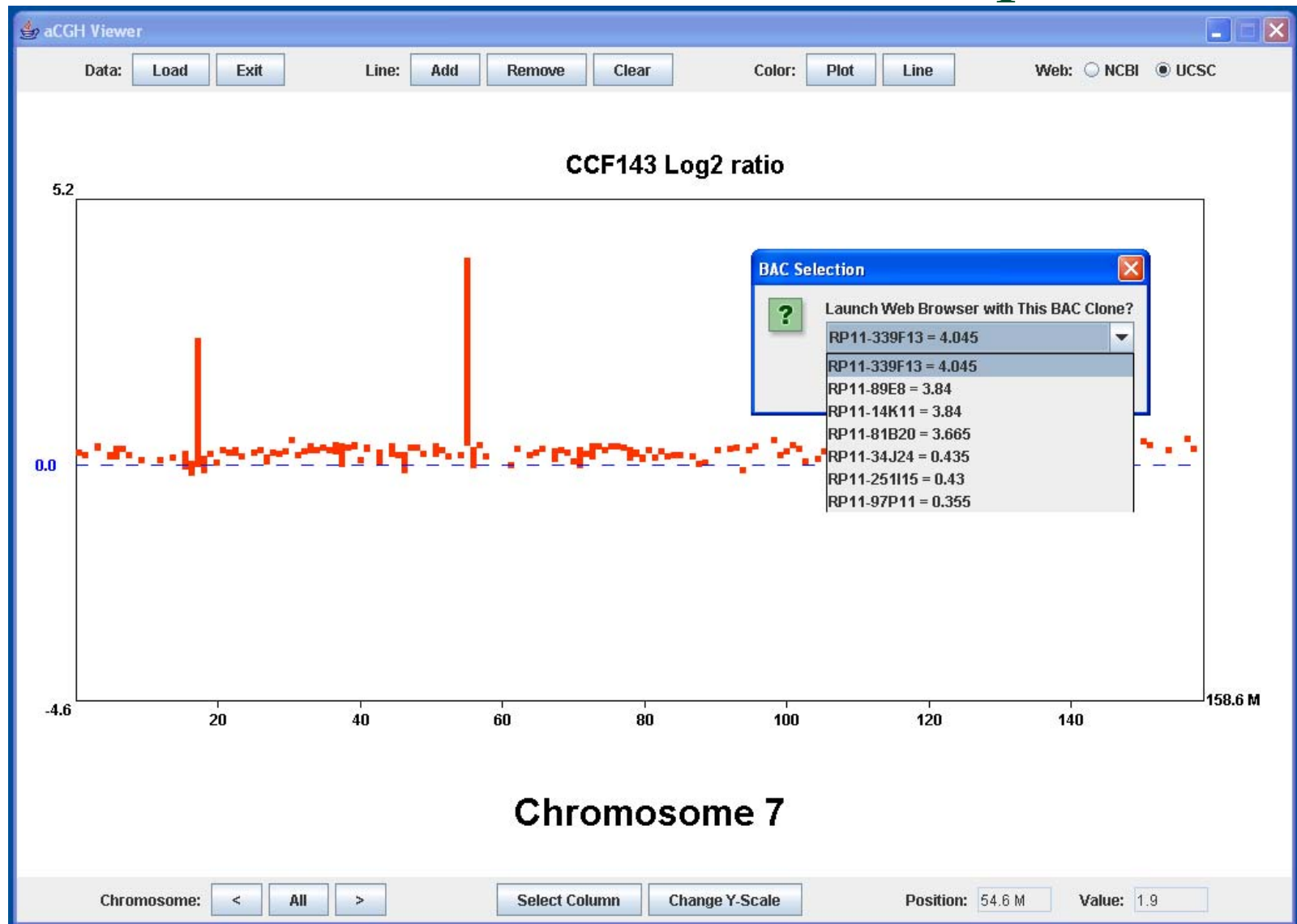
# Adding a threshold line







# Information for individual data points



# Link to genome browser by BAC ID

Human chr7:55,029,594-55,154,846 - UCSC Genome Browser v100 - Microsoft Internet Explorer provided by RPCI Information Technology

File Edit View Favorites Tools Help

Back Forward Stop Refresh Home Search Favorites Media History Mail Print Edit

Address <http://genome.ucsc.edu/cgi-bin/hgTracks> Go Links

Home Genomes Blat PCR DNA Tables Gene Sorter Convert Ensembl NCBI PDF/PS Help

## UCSC Genome Browser on Human May 2004 Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x

position chr7:55,029,594-55,154,846 jump clear size 125,253 bp. configure

chr7 (p11.2) p21.3 p21.1 p15.3 14.3 p14.1 p13 11.23 7q21.11 21.3 q22.1 7q31.1 7q33 7q34 q35 36.1

Base Position 55040000 55050000 55060000 55070000 55080000 55090000 55100000 55110000 55120000 55130000 55140000 5

Chromosome Band 7p11.2

STS Markers on Genetic (blue) and Radiation Hybrid (black) Maps

Clones Placed on Cytogenetic Map Using FISH

Gap Locations

BAC End Pairs

Known Genes (Nov 22, 04) Based on SWISS-PROT, TrEMBL, mRNA, and RefSeq

Consensus CDS

RefSeq Genes

Ensembl Gene Predictions

GeneView Gene Models With Alt-Splicing

GeneScan Gene Predictions

Human mRNAs from GenBank

EGFR

CCDS

EGFR

Ensembl Genes

Assembly Genes

NT\_033968.94

NT\_033968.95

NT\_033968.96

NT\_033968.97

K03193

X00530

BC070881

K03193

X00530

AK123474

CR618371

CR603510

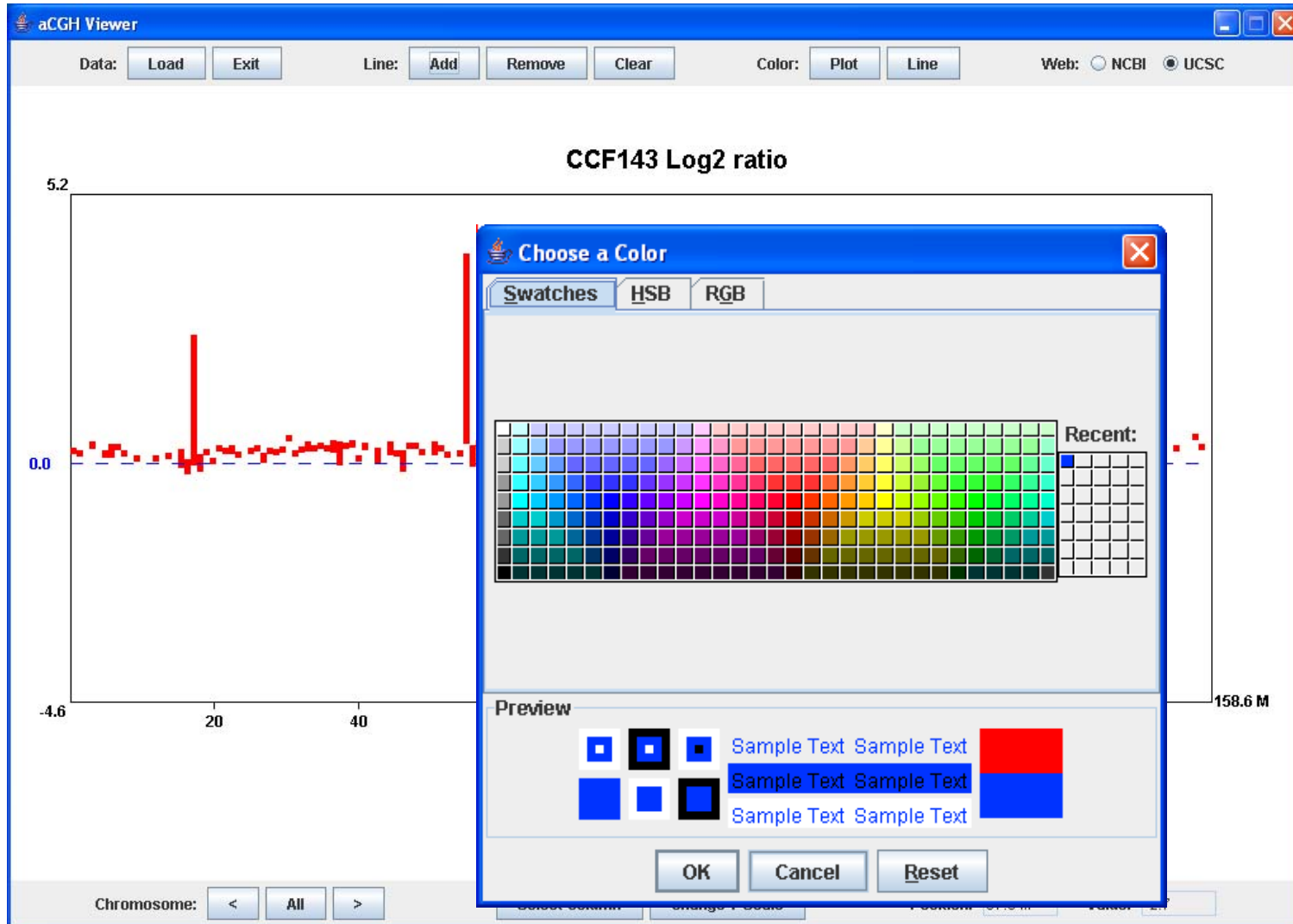
U51732

AK026818

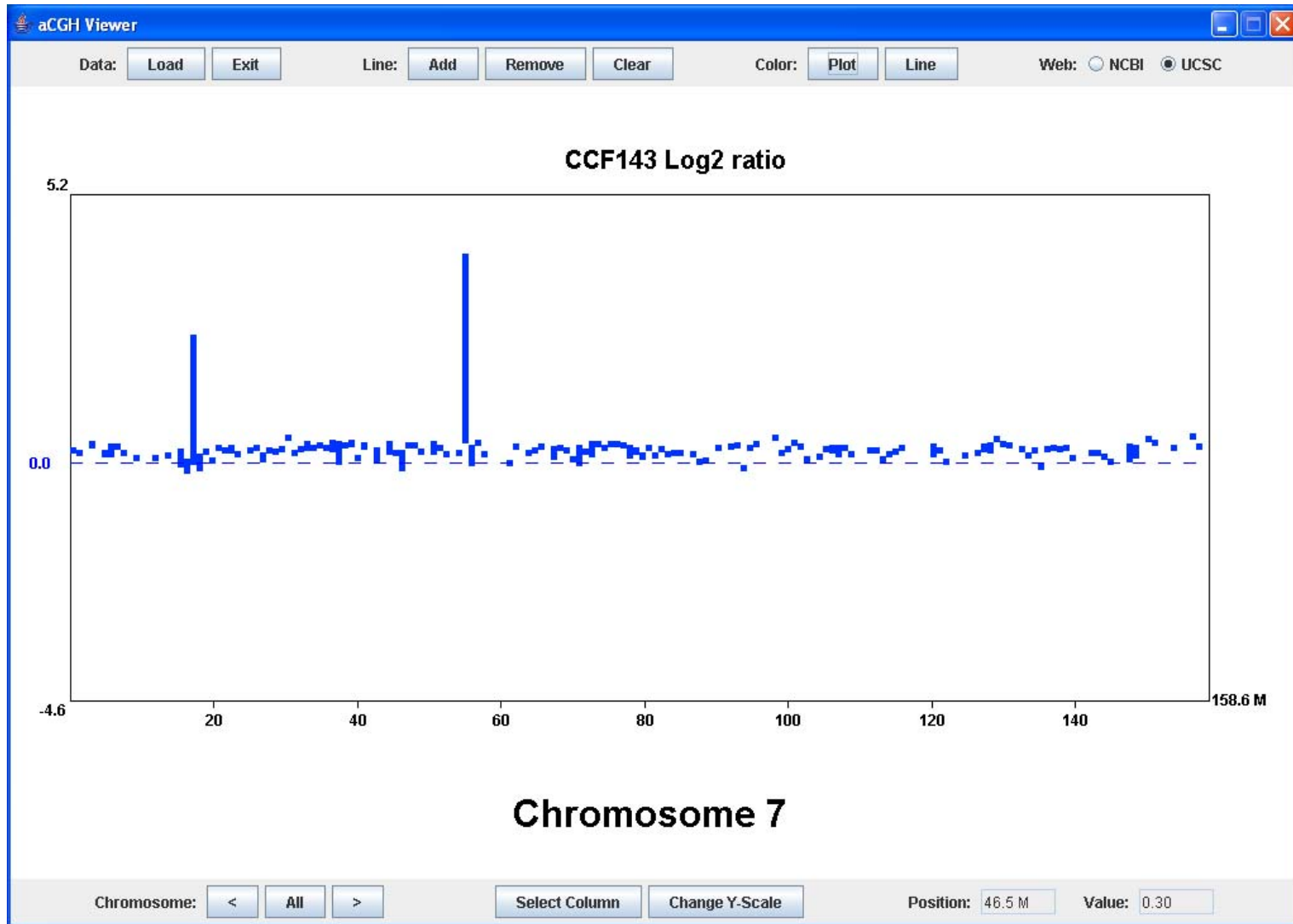
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AK130364

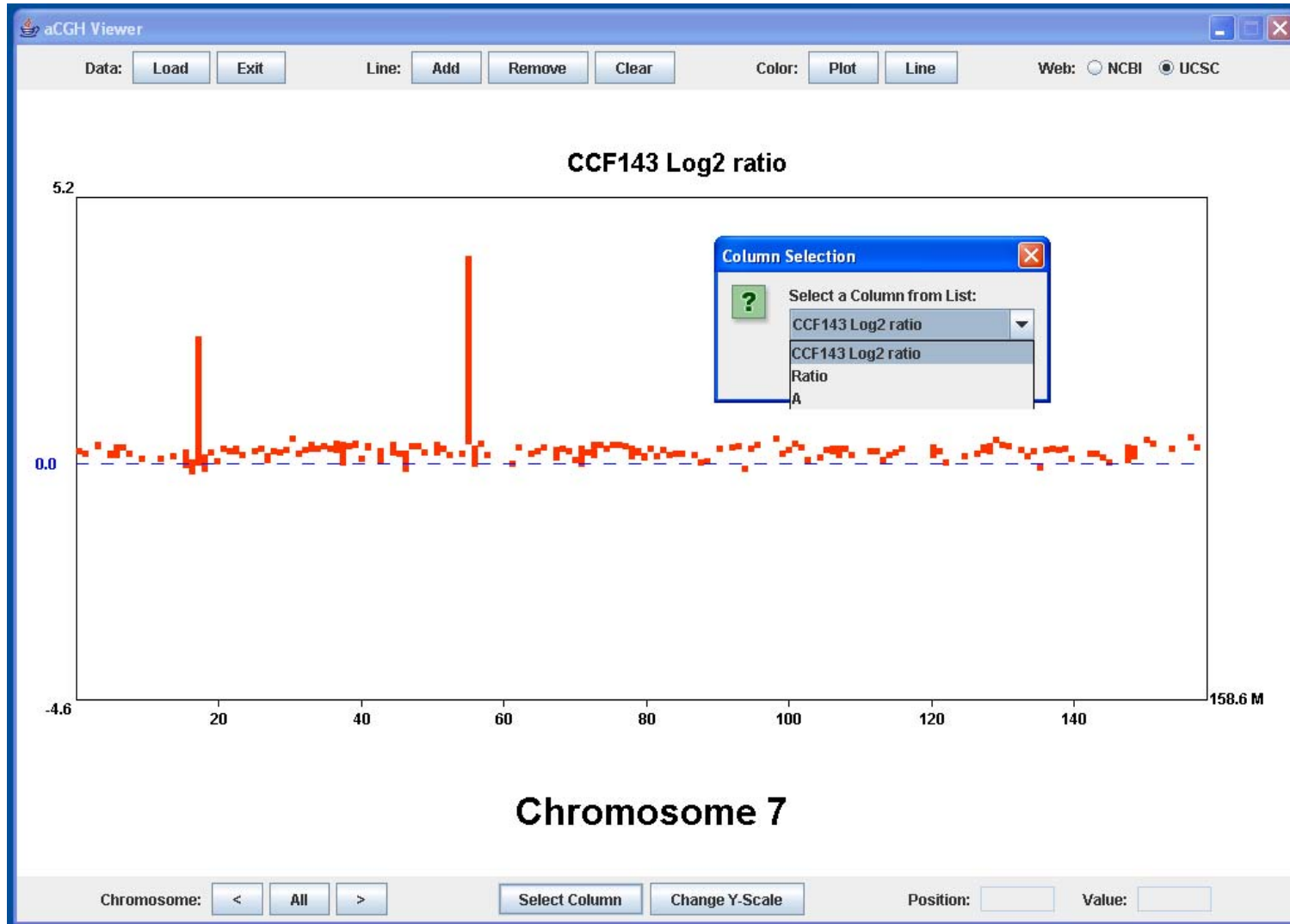
# Changing plot color



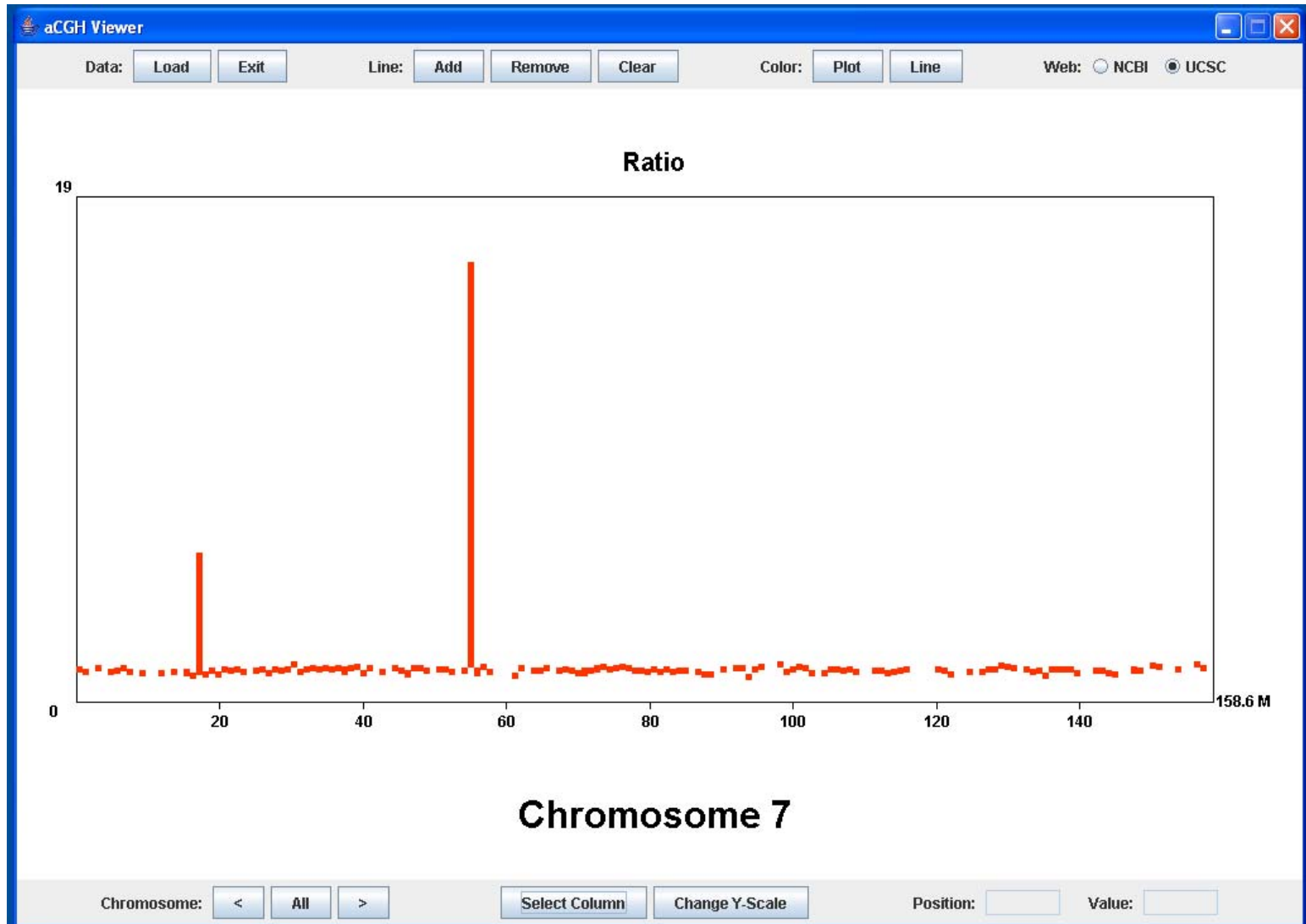
# Changing plot color (cont'd)



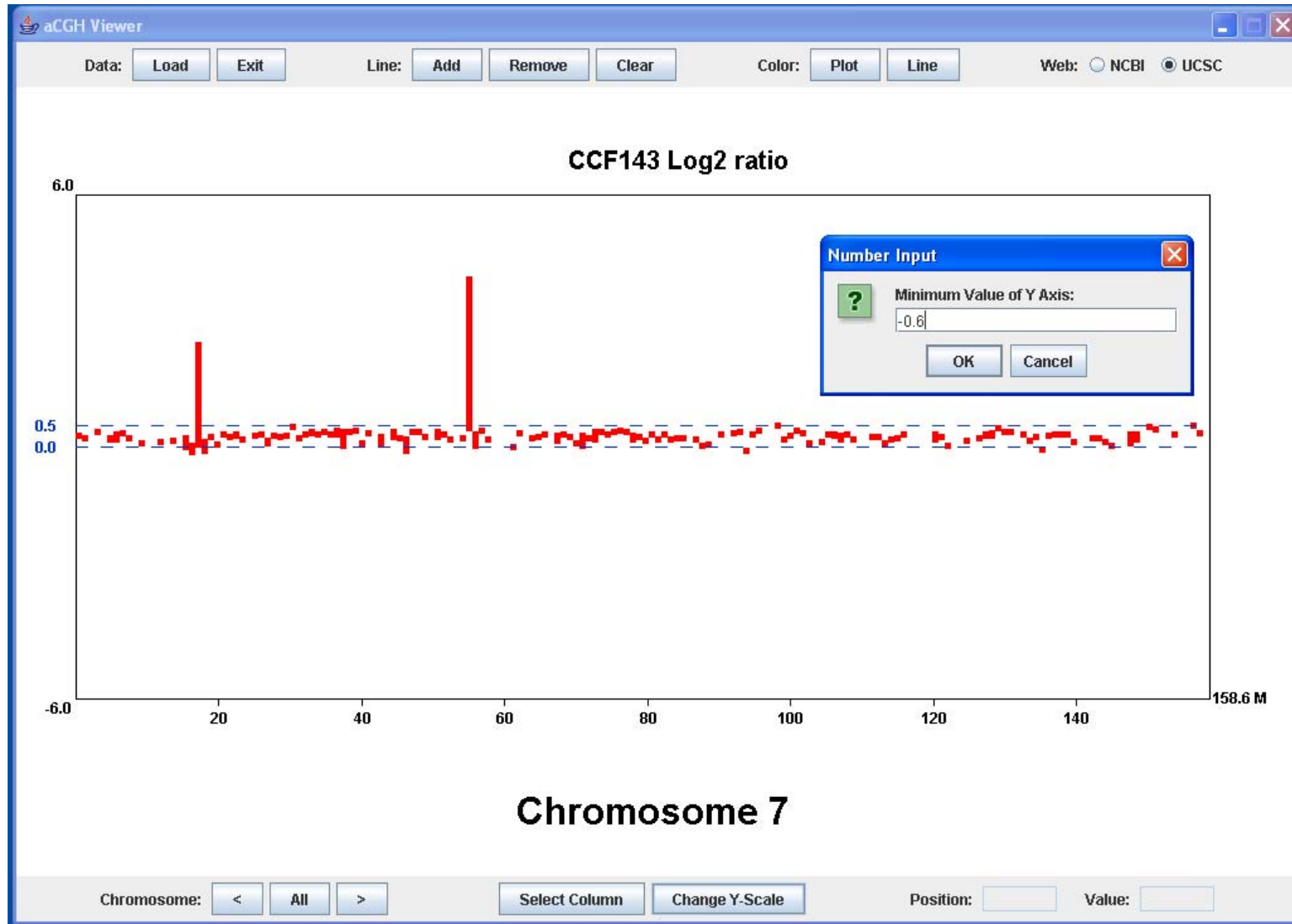
# Select different data to plot



# Select different data to plot (cont'd)

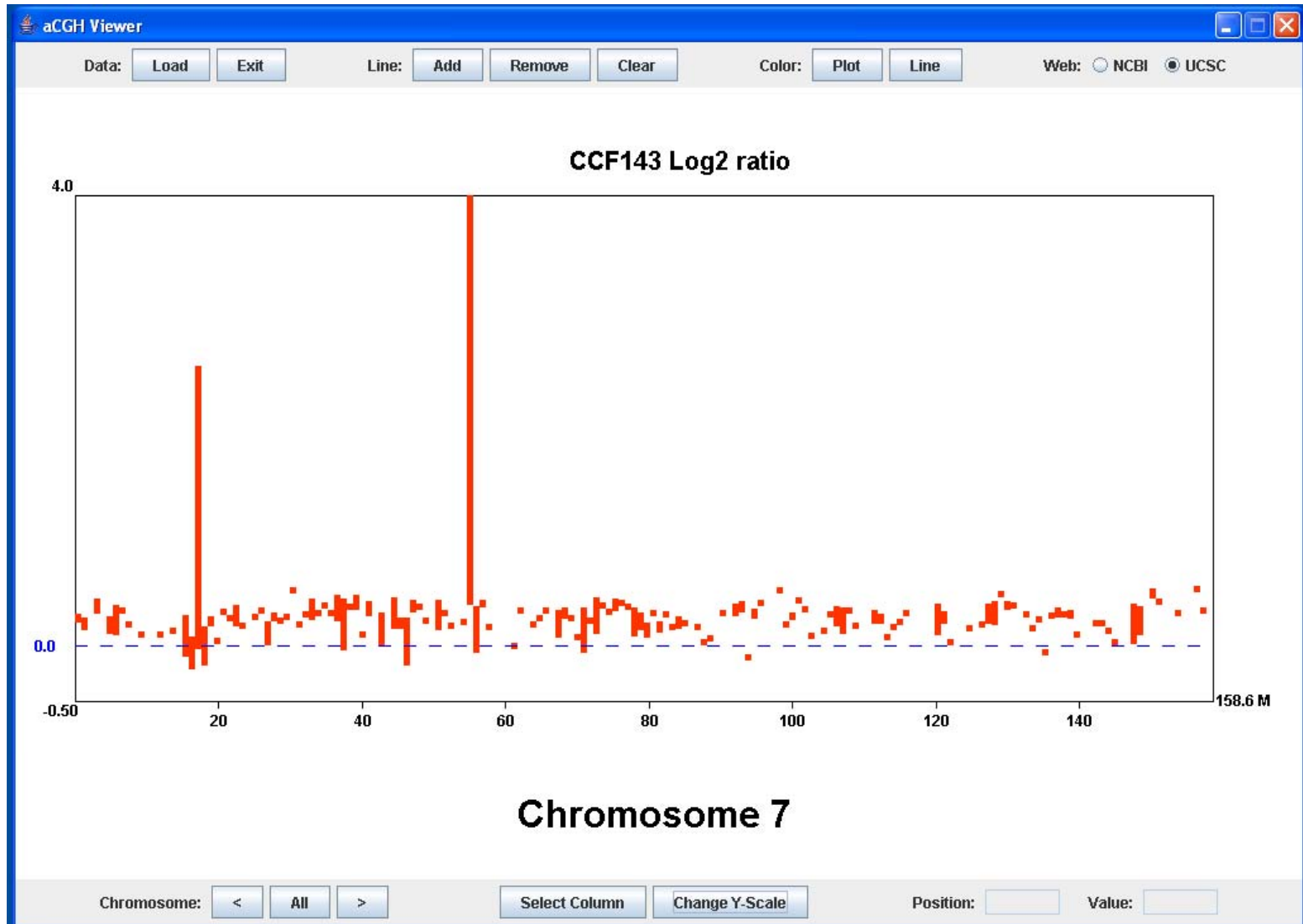


# Adjusting Y-axis scale





# Adjusting Y-axis scale (cont'd)



# Functions to be implemented

- Interface for data selection and labeling, selection of filter, image printing
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Thank you and we  
appreciate your comments

# Questions for discussions

- Standalone application vs. web application
- Standardization of input data
- Are there any similar tools being developed at CaBIG?
- If not, what would be the expectations for aCGH Viewer to be included as an CaBIG tool?